

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: COHEN, CHARLES M.
CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.

(ii) TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
ULCERS

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CREATIVE BIOMOLECULES
(B) STREET: 35 SOUTH STREET
(C) CITY: HOPKINTON
(D) STATE: MASSACHUSETTS
(E) COUNTRY: U.S.A.
(F) ZIP: 01748

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 667,274
(B) FILING DATE: 11-MAR-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 752,764
(B) FILING DATE: 30-AUG-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 753,059
(B) FILING DATE: 30-AUG-1991

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME: Generic Sequence 1
 (D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 Xaa Xaa Xaa Xaa Xaa Xaa
 1 5
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 20 25
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 30 35
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 40 45 50
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55 60
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 85 90
 Xaa Cys Xaa
 95

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: Generic Sequence 2
 (D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Xaa Xaa Xaa Xaa Xaa
 1 5
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 20 25
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 30 35
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 40 45 50

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
                    55                      60
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                    65                      70
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                    75                      80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
                    85                      90
Xaa Cys Xaa
                    95

```

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: Generic Sequence 3
 - (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

      Leu Tyr Val Xaa Phe
        1             5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
          10
Xaa Ala Pro Gly Xaa Xaa Xaa Ala
   15             20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
          25             30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
          35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
          40             45
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
          50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
          55             60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
          65
Xaa Xaa Xaa Leu Xaa Xaa Xaa
          70             75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
          80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
          85             90
Xaa Cys Gly Cys Xaa
          95

```

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: Generic Sequence 4
 - (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Cys Xaa Xaa Xaa Xaa Leu Tyr Val Xaa Phe
 1               5              10
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
              15
Xaa Ala Pro Xaa Gly Xaa Xaa Ala
 20           25
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
           30           35
Xaa Pro Xaa Xaa Xaa Xaa Xaa
              40
XXa Asn Xaa Xaa Asn His Ala Xaa Xaa
           45           50
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
              55
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
           60           65
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
              70
Xaa Xaa Xaa Leu Xaa Xaa Xaa
           75           80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
              85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
           90           95
Xaa Cys Gly Cys Xaa
              100
  
```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: hOP-1 (mature form)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser 1	Thr	Gly	Ser	Lys 5	Gln	Arg	Ser	Gln
Asn 10	Arg	Ser	Lys	Thr	Pro 15	Lys	Asn	Gln
Glu 20	Ala	Leu	Arg	Met	Ala	Asn 25	Val	Ala
Glu	Asn	Ser 30	Ser	Ser	Asp	Gln	Arg 35	Gln
Ala	Cys	Lys	Lys 40	His	Glu	Leu	Tyr	Val 45
Ser	Phe	Arg	Asp	Leu 50	Gly	Trp	Gln	Asp
Trp 55	Ile	Ile	Ala	Pro	Glu 60	Gly	Tyr	Ala
Ala	Tyr 65	Tyr	Cys	Glu	Gly	Glu 70	Cys	Ala
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn 80	Ala
Thr	Asn	His	Ala 85	Ile	Val	Gln	Thr	Leu 90
Val	His	Phe	Ile	Asn 95	Pro	Glu	Thr	Val
Pro 100	Lys	Pro	Cys	Cys	Ala 105	Pro	Thr	Gln
Leu	Asn 110	Ala	Ile	Ser	Val	Leu 115	Tyr	Phe
Asp	Asp	Ser 120	Ser	Asn	Val	Ile	Leu 125	Lys
Lys	Tyr	Arg	Asn 130	Met	Val	Val	Arg	Ala 135
Cys	Gly	Cys	His					

(2)

INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: mOP-1 (mature form)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser 1	Thr	Gly	Gly	Lys 5	Gln	Arg	Ser	Gln
Asn 10	Arg	Ser	Lys	Thr	Pro 15	Lys	Asn	Gln
Glu 20	Ala	Leu	Arg	Met	Ala	Ser 25	Val	Ala
Glu	Asn	Ser 30	Ser	Ser	Asp	Gln	Arg 35	Gln
Ala	Cys	Lys	Lys 40	His	Glu	Leu	Tyr	Val 45

Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
				50				
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Asp	Thr	Val
				95				
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

(2)

INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: hOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90

Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100				105				
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: mOP-2 (mature form)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10				15				
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
			50					
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55				60				
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
			95					
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100				105				
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: CBMP-2A(fx)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser
1				5					10	
Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro
		15						20		
Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	Gly	Glu
		25					30			
Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser
	35					40				
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn
45				50					55	
Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys
			60						65	
Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu
		70						75		
Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys
	80						85			
Asn	Tyr	Gln	Asp	Met	Val	Val	Glu	Gly	Cys	Gly
	90				95					
Cys	Arg									
100										

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: CBMP-2B(fx)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

								Cys	Arg	Arg	His	Ser
								1				5
Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn		
				10					15			
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala		
		20						25				
Phe	Tyr	Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu		
		30					35					
Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile		
	40					45						
Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser		
50					55					60		

Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu
				65					70	
Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Tyr
			75					80		
Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met
		85				90				
Val	Val	Glu	Gly	Cys	Gly	Cys	Arg			
		95				100				

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: DPP(fx)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser
1				5					10	
Asp	Val	Gly	Trp	Asp	Asp	Trp	Ile	Val	Ala	Pro
			15					20		
Leu	Gly	Tyr	Asp	Ala	Tyr	Tyr	Cys	His	Gly	Lys
		25					30			
Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Phe	Asn	Ser
	35					40				
Thr	Asn	His	Ala	Val	Val	Gln	Thr	Leu	Val	Asn
45					50					55
Asn	Asn	Asn	Pro	Gly	Lys	Val	Pro	Lys	Ala	Cys
				60					65	
Cys	Val	Pro	Thr	Gln	Leu	Asp	Ser	Val	Ala	Met
			70					75		
Leu	Tyr	Leu	Asn	Asp	Gln	Ser	Thr	Val	Val	Leu
		80					85			
Lys	Asn	Tyr	Gln	Glu	Met	Thr	Val	Val	Gly	Cys
	90					95				
Gly	Cys	Arg								
100										

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: Vgl(fx)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys	Lys	Lys	Arg	His	Leu	Tyr	Val	Glu	Phe	Lys
1				5					10	
Asp	Val	Gly	Trp	Gln	Asn	Trp	Val	Ile	Ala	Pro
			15					20		

Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu
 25 30
 Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly
 35 40
 Ser Asn His Ala Ile Leu Gln Thr Leu Val His
 45 50 55
 Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys
 60 65
 Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met
 70 75
 Leu Phe Tyr Asp Asn Asn Asp Asn Val Val Leu
 80 85
 Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys
 90 95
 Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Vgr-1(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln
 1 5 10
 Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro
 15 20
 Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu
 25 30
 Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
 35 40
 Thr Asn His Ala Ile Val Gln Thr Leu Val His
 45 50 55
 Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys
 60 65
 Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val
 70 75
 Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu
 80 85
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys
 90 95
 Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: human
(F) TISSUE TYPE: BRAIN

(ix) FEATURE:
(D) OTHER INFORMATION:
/product= "GDF-1 (fx)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	
1				5					10					
Trp	His	Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr
15				20					25					
Cys	Gln	Gly	Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly
30				35					40					
Gly	Pro	Pro	Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His
45				50					55					
Ala	Ala	Ala	Pro	Gly	Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala
60				65					70					
Arg	Leu	Ser	Pro	Ile	Ser	Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn
75				80					85					
Val	Val	Leu	Arg	Gln	Tyr	Glu	Asp	Met	Val	Val	Asp	Glu	Cys	Gly
90				95					100					
Cys	Arg													
105														

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys	Xaa	Xaa	Xaa	Xaa
1				5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 49..1341
- (D) OTHER INFORMATION:/standard_name= "hOP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG	ATG CAC GTG	57
	Met His Val	
	1	
CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA		105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala		
5 10 15		
CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC		153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn		
20 25 30 35		
GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG		201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg		
40 45 50		
CGG GAG ATG CAG CGG GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC		249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg		
55 60 65		
CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG		297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met		
70 75 80		
CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC		345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly		
85 90 95		
GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC		393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly		
100 105 110 115		

CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	441
Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
				120					125					130		
ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	489
Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
			135					140					145			
CAC	CCA	CGC	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	537
His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
			150				155					160				
CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	585
Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
	165					170					175					
TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	633
Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
180					185					190					195	
CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
				200					205					210		
GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
			215					220					225			
ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
		230					235					240				
GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
	245					250					255					
AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
260					265					270					275	
TTC	ATG	GTG	GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	921
Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	
				280					285					290		
CGG	TCC	ACG	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	969
Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	
			295					300					305			
AAG	AAC	CAG	GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	1017
Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	
		310					315					320				

AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	1065
Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
325 330 335	
CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC	1113
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
340 345 350 355	
GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG	1161
Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
360 365 370	
AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC	1209
Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
375 380 385	
CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC	1257
Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	
390 395 400	
ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA	1305
Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys	
405 410 415	
TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC	1351
Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
420 425 430	
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC	1531
ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGC AAAACC TAGCAGGAAA AAAAAACAAC	1591
GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT	1651
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC	1771
CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAAA AAAAAAAAAA A	1822

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(D) OTHER INFORMATION: /Product="OP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met 1	His	Val	Arg	Ser 5	Leu	Arg	Ala	Ala	Ala 10	Pro	His	Ser	Phe	Val 15	Ala
Leu	Trp	Ala	Pro 20	Leu	Phe	Leu	Leu	Arg 25	Ser	Ala	Leu	Ala	Asp 30	Phe	Ser
Leu	Asp	Asn 35	Glu	Val	His	Ser	Ser 40	Phe	Ile	His	Arg	Arg 45	Leu	Arg	Ser
Gln	Glu 50	Arg	Arg	Glu	Met	Gln 55	Arg	Glu	Ile	Leu	Ser 60	Ile	Leu	Gly	Leu
Pro 65	His	Arg	Pro	Arg	Pro 70	His	Leu	Gln	Gly	Lys 75	His	Asn	Ser	Ala	Pro 80
Met	Phe	Met	Leu	Asp 85	Leu	Tyr	Asn	Ala	Met 90	Ala	Val	Glu	Glu	Gly 95	Gly
Gly	Pro	Gly	Gly 100	Gln	Gly	Phe	Ser	Tyr 105	Pro	Tyr	Lys	Ala	Val 110	Phe	Ser
Thr	Gln	Gly 115	Pro	Pro	Leu	Ala	Ser 120	Leu	Gln	Asp	Ser	His 125	Phe	Leu	Thr
Asp	Ala 130	Asp	Met	Val	Met	Ser 135	Phe	Val	Asn	Leu	Val 140	Glu	His	Asp	Lys
Glu 145	Phe	Phe	His	Pro	Arg 150	Tyr	His	His	Arg	Glu 155	Phe	Arg	Phe	Asp	Leu 160
Ser	Lys	Ile	Pro	Glu 165	Gly	Glu	Ala	Val	Thr 170	Ala	Ala	Glu	Phe	Arg 175	Ile
Tyr	Lys	Asp 180	Tyr	Ile	Arg	Glu	Arg	Phe 185	Asp	Asn	Glu	Thr	Phe 190	Arg	Ile
Ser	Val	Tyr 195	Gln	Val	Leu	Gln	Glu 200	His	Leu	Gly	Arg	Glu 205	Ser	Asp	Leu
Phe 210	Leu	Leu	Asp	Ser	Arg	Thr 215	Leu	Trp	Ala	Ser	Glu 220	Glu	Gly	Trp	Leu
Val 225	Phe	Asp	Ile	Thr	Ala 230	Thr	Ser	Asn	His	Trp 235	Val	Val	Asn	Pro	Arg 240
His	Asn	Leu	Gly 245	Leu	Gln	Leu	Ser	Val	Glu 250	Thr	Leu	Asp	Gly	Gln 255	Ser

Ile	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	
			260					265					270			
Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	
		275					280					285				
Arg	Ser	Ile	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	
	290					295					300					
Lys	Thr	Pro	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	
305					310					315					320	
Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	
				325					330					335		
Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	
			340					345					350			
Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	
		355					360					365				
Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	
	370					375					380					
Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	
385					390					395					400	
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	
				405					410					415		
Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His		
			420				425						430			

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: MURIDAE
 - (F) TISSUE TYPE: EMBRYO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 104..1393
 - (D) OTHER INFORMATION: /note= "MOP1 (CDNA)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG															60	
CGGCGCGGGC CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC Met His Val Arg 1															115	
TCG Ser 5	CTG Leu	CGC Arg	GCT Ala	GCG Ala	GCG Ala 10	CCA Pro	CAC His	AGC Ser	TTC Phe	GTG Val 15	GCG Ala	CTC Leu	TGG Trp	GCG Ala	CCT Pro 20	163
CTG Leu	TTC Phe	TTG Leu	CTG Leu	CGC Arg 25	TCC Ser	GCC Ala	CTG Leu	GCC Ala	GAT Asp 30	TTC Phe	AGC Ser	CTG Leu	GAC Asp	AAC Asn 35	GAG Glu	211
GTG Val	CAC His	TCC Ser	AGC Ser 40	TTC Phe	ATC Ile	CAC His	CGG Arg	CGC Arg 45	CTC Leu	CGC Arg	AGC Ser	CAG Gln	GAG Glu 50	CGG Arg	CGG Arg	259
GAG Glu	ATG Met	CAG Gln 55	CGG Arg	GAG Glu	ATC Ile	CTG Leu	TCC Ser 60	ATC Ile	TTA Leu	GGG Gly	TTG Leu	CCC Pro 65	CAT His	CGC Arg	CCG Pro	307
CGC Arg 70	CCG Pro	CAC His	CTC Leu	CAG Gln	GGA Gly 75	AAG Lys	CAT His	AAT Asn	TCG Ser	GCG Ala	CCC Pro 80	ATG Met	TTC Phe	ATG Met	TTG Leu	355
GAC Asp 85	CTG Leu	TAC Tyr	AAC Asn	GCC Ala	ATG Met 90	GCG Ala	GTG Val	GAG Glu	GAG Glu	AGC Ser 95	GGG Gly	CCG Pro	GAC Asp	GGA Gly	CAG Gln 100	403
GGC Gly	TTC Phe	TCC Ser	TAC Tyr	CCC Pro 105	TAC Tyr	AAG Lys	GCC Ala	GTC Val	TTC Phe 110	AGT Ser	ACC Thr	CAG Gln	GGC Gly	CCC Pro 115	CCT Pro	451
TTA Leu	GCC Ala	AGC Ser	CTG Leu 120	CAG Gln	GAC Asp	AGC Ser	CAT His	TTC Phe 125	CTC Leu	ACT Thr	GAC Asp	GCC Ala	GAC Asp 130	ATG Met	GTC Val	499
ATG Met	AGC Ser	TTC Phe 135	GTC Val	AAC Asn	CTA Leu	GTG Val	GAA Glu 140	CAT His	GAC Asp	AAA Lys	GAA Glu 145	TTC Phe 145	TTC Phe	CAC His	CCT Pro	547
CGA Arg	TAC Tyr 150	CAC His	CAT His	CGG Arg	GAG Glu	TTC Phe 155	CGG Arg	TTT Phe	GAT Asp	CTT Leu	TCC Ser 160	AAG Lys	ATC Ile	CCC Pro	GAG Glu	595
GGC Gly 165	GAA Glu	CGG Arg	GTG Val	ACC Thr 170	GCA Ala	GCC Ala	GAA Glu	TTC Phe	AGG Arg	ATC Ile 175	TAT Tyr	AAG Lys	GAC Asp	TAC Tyr	ATC Ile 180	643
CGG Arg	GAG Glu	CGA Arg	TTT Phe	GAC Asp 185	AAC Asn	GAG Glu	ACC Thr	TTC Phe	CAG Gln 190	ATC Ile	ACA Thr	GTC Val	TAT Tyr	CAG Gln 195	GTG Val	691

CTC	CAG	GAG	CAC	TCA	GGC	AGG	GAG	TCG	GAC	CTC	TTC	TTG	CTG	GAC	AGC	739
Leu	Gln	Glu	His	Ser	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	
			200					205					210			
CGC	ACC	ATC	TGG	GCT	TCT	GAG	GAG	GGC	TGG	TTG	GTG	TTT	GAT	ATC	ACA	787
Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	
		215					220					225				
GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAC	CCT	CGG	CAC	AAC	CTG	GGC	TTA	835
Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu	
	230					235					240					
CAG	CTC	TCT	GTG	GAG	ACC	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	AAG	TTG	883
Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu	
	245				250					255					260	
GCA	GGC	CTG	ATT	GGA	CGG	CAT	GGA	CCC	CAG	AAC	AAG	CAA	CCC	TTC	ATG	931
Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met	
			265					270						275		
GTG	GCC	TTC	TTC	AAG	GCC	ACG	GAA	GTC	CAT	CTC	CGT	AGT	ATC	CGG	TCC	979
Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg	Ser	Ile	Arg	Ser	
			280					285					290			
ACG	GGG	GGC	AAG	CAG	CGC	AGC	CAG	AAT	CGC	TCC	AAG	ACG	CCA	AAG	AAC	1027
Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	
		295					300					305				
CAA	GAG	GCC	CTG	AGG	ATG	GCC	AGT	GTG	GCA	GAA	AAC	AGC	AGC	AGT	GAC	1075
Gln	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	
	310					315					320					
CAG	AGG	CAG	GCC	TGC	AAG	AAA	CAT	GAG	CTG	TAC	GTC	AGC	TTC	CGA	GAC	1123
Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	
	325				330					335					340	
CTT	GGC	TGG	CAG	GAC	TGG	ATC	ATT	GCA	CCT	GAA	GGC	TAT	GCT	GCC	TAC	1171
Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	
			345						350					355		
TAC	TGT	GAG	GGA	GAG	TGC	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	AAC	GCC	1219
Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	
			360					365					370			
ACC	AAC	CAC	GCC	ATC	GTC	CAG	ACA	CTG	GTT	CAC	TTC	ATC	AAC	CCA	GAC	1267
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Asp	
		375					380					385				
ACA	GTA	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACC	CAG	CTC	AAC	GCC	ATC	TCT	1315
Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	
	390					395					400					

GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
405 410 415 420	
AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG	1413
Asn Met Val Val Arg Ala Cys Gly Cys His	
425 430	
ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
GGCAGGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
AATCGCAAGC CTCGTTGAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCGCTGGCG	1773
TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC	1873

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (D) OTHER INFORMATION: /product= "mOP1-PP"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala	
1 5 10 15	
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser	
20 25 30	
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser	
35 40 45	
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu	
50 55 60	
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro	
65 70 75 80	

Met	Phe	Met	Leu	Asp 85	Leu	Tyr	Asn	Ala	Met 90	Ala	Val	Glu	Glu	Ser 95	Gly
Pro	Asp	Gly	Gln 100	Gly	Phe	Ser	Tyr	Pro 105	Tyr	Lys	Ala	Val	Phe 110	Ser	Thr
Gln	Gly	Pro 115	Pro	Leu	Ala	Ser	Leu 120	Gln	Asp	Ser	His	Phe 125	Leu	Thr	Asp
Ala	Asp	Met	Val	Met	Ser	Phe 135	Val	Asn	Leu	Val	Glu 140	His	Asp	Lys	Glu
Phe 145	Phe	His	Pro	Arg	Tyr 150	His	His	Arg	Glu	Phe 155	Arg	Phe	Asp	Leu	Ser 160
Lys	Ile	Pro	Glu	Gly 165	Glu	Arg	Val	Thr	Ala 170	Ala	Glu	Phe	Arg	Ile 175	Tyr
Lys	Asp	Tyr 180	Ile	Arg	Glu	Arg	Phe	Asp 185	Asn	Glu	Thr	Phe	Gln 190	Ile	Thr
Val	Tyr	Gln 195	Val	Leu	Gln	Glu	His 200	Ser	Gly	Arg	Glu	Ser 205	Asp	Leu	Phe
Leu 210	Leu	Asp	Ser	Arg	Thr	Ile 215	Trp	Ala	Ser	Glu	Glu 220	Gly	Trp	Leu	Val
Phe 225	Asp	Ile	Thr	Ala	Thr 230	Ser	Asn	His	Trp	Val 235	Val	Asn	Pro	Arg	His 240
Asn	Leu	Gly	Leu	Gln 245	Leu	Ser	Val	Glu	Thr 250	Leu	Asp	Gly	Gln	Ser 255	Ile
Asn	Pro	Lys	Leu 260	Ala	Gly	Leu	Ile	Gly 265	Arg	His	Gly	Pro	Gln 270	Asn	Lys
Gln	Pro	Phe 275	Met	Val	Ala	Phe	Phe 280	Lys	Ala	Thr	Glu	Val 285	His	Leu	Arg
Ser	Ile 290	Arg	Ser	Thr	Gly	Gly 295	Lys	Gln	Arg	Ser	Gln 300	Asn	Arg	Ser	Lys
Thr 305	Pro	Lys	Asn	Gln	Glu 310	Ala	Leu	Arg	Met	Ala 315	Ser	Val	Ala	Glu	Asn 320
Ser	Ser	Ser	Asp	Gln 325	Arg	Gln	Ala	Cys	Lys 330	Lys	His	Glu	Leu	Tyr 335	Val
Ser	Phe	Arg	Asp 340	Leu	Gly	Trp	Gln	Asp 345	Trp	Ile	Ile	Ala	Pro 350	Glu	Gly

Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser
 355 360 365

Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe
 370 375 380

Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400

Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415

Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:20:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii)MOLECULE TYPE: cDNA

(vi)ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix)FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 490..1696
- (D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCGCCGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA	60
GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCAGG AGGCGCTGGA GCAACAGCTC	120
CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCCATC GCCCCTGCGC TGCTCGGACC	180
GCGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT	240
CCGCAGAGTA GCCCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG	300
GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC	360
CGCCCCGCCC CGCCGCCCGC CGCCGCCGA GCCCAGCCTC CTTGCCGTCG GGGCGTCCCC	420
AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480

CGGCCTGCC	ATG	ACC	GCG	CTC	CCC	GGC	CCG	CTC	TGG	CTC	CTG	GGC	CTG		528
	Met	Thr	Ala	Leu	Pro	Gly	Pro	Leu	Trp	Leu	Leu	Gly	Leu		
	1				5				10						
GCG	CTA	TGC	GCG	CTG	GGC	GGG	GGC	GGC	CCC	GGC	CTG	CGA	CCC	CCG	576
Ala	Leu	Cys	Ala	Leu	Gly	Gly	Gly	Gly	Pro	Gly	Leu	Arg	Pro	Pro	
	15				20				25						
GGC	TGT	CCC	CAG	CGA	CGT	CTG	GGC	GCG	CGC	GAG	CGC	CGG	GAC	GTG	624
Gly	Cys	Pro	Gln	Arg	Arg	Leu	Gly	Ala	Arg	Glu	Arg	Arg	Asp	Val	
	30				35				40					45	
CGC	GAG	ATC	CTG	GCG	GTG	CTC	GGG	CTG	CCT	GGG	CGG	CCC	CGG	CCC	672
Arg	Glu	Ile	Leu	Ala	Val	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Arg	Pro	
				50					55					60	
GCG	CCA	CCC	GCC	GCC	TCC	CGG	CTG	CCC	GCG	TCC	GCG	CCG	CTC	TTC	720
Ala	Pro	Pro	Ala	Ala	Ser	Arg	Leu	Pro	Ala	Ser	Ala	Pro	Leu	Phe	
			65				70						75	Met	
CTG	GAC	CTG	TAC	CAC	GCC	ATG	GCC	GGC	GAC	GAC	GAC	GAG	GAC	GGC	768
Leu	Asp	Leu	Tyr	His	Ala	Met	Ala	Gly	Asp	Asp	Asp	Glu	Asp	Gly	
		80					85					90		Ala	
CCC	GCG	GAG	CGG	CGC	CTG	GGC	CGC	GCC	GAC	CTG	GTC	ATG	AGC	TTC	816
Pro	Ala	Glu	Arg	Arg	Leu	Gly	Arg	Ala	Asp	Leu	Val	Met	Ser	Phe	
	95					100					105			Val	
AAC	ATG	GTG	GAG	CGA	GAC	CGT	GCC	CTG	GGC	CAC	CAG	GAG	CCC	CAT	864
Asn	Met	Val	Glu	Arg	Asp	Arg	Ala	Leu	Gly	His	Gln	Glu	Pro	His	
	110				115					120				Trp	
AAG	GAG	TTC	CGC	TTT	GAC	CTG	ACC	CAG	ATC	CCG	GCT	GGG	GAG	GCG	912
Lys	Glu	Phe	Arg	Phe	Asp	Leu	Thr	Gln	Ile	Pro	Ala	Gly	Glu	Ala	
				130					135					140	
ACA	GCT	GCG	GAG	TTC	CGG	ATT	TAC	AAG	GTG	CCC	AGC	ATC	CAC	CTG	960
Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Val	Pro	Ser	Ile	His	Leu	
			145					150					155	Leu	
AAC	AGG	ACC	CTC	CAC	GTC	AGC	ATG	TTC	CAG	GTG	GTC	CAG	GAG	CAG	1008
Asn	Arg	Thr	Leu	His	Val	Ser	Met	Phe	Gln	Val	Val	Gln	Glu	Gln	
		160					165					170		Ser	
AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	CTT	CAG	ACG	CTC	CGA	1056
Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	Leu	Gln	Thr	Leu	Arg	
	175				180						185			Ala	
GGA	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAT	GTC	ACA	GCA	GCC	AGT	GAC	1104
Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Val	Thr	Ala	Ala	Ser	Asp	
	190				195				200					Cys	

TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG	1152
Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu	
210 215 220	
ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT	1200
Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly	
225 230 235	
CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG	1248
Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg	
240 245 250	
GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG	1296
Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg	
255 260 265	
AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC	1344
Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu	
270 275 280 285	
CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC	1392
Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys	
290 295 300	
CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC	1440
Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp	
305 310 315	
TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG	1488
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu	
320 325 330	
TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC	1536
Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile	
335 340 345	
CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG	1584
Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala	
350 355 360 365	
TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC	1632
Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp	
370 375 380	
AGC AGC AAC AAC GTC ATC CTG CGC AAA CAC CGC AAC ATG GTG GTC AAG	1680
Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys	
385 390 395	
GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG	1723
Ala Cys Gly Cys His	
400	

(2) INFORMATION FOR SEQ ID NO:21:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

- (A)OTHER INFORMATION: /product= "hOP2-PP"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1           5           10           15

Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro
          20           25           30

Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile
          35           40           45

Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
          50           55           60

Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
          65           70           75           80

Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
          85           90           95

Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
          100          105          110

Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
          115          120          125

Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala
          130          135          140

Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr
          145          150          155          160

Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu
          165          170          175

Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu
          180          185          190

Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu
          195          200          205

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Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp
 210 215 220
 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala
 225 230 235 240
 Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro
 245 250 255
 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln
 260 265 270
 Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile
 275 280 285
 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His
 290 295 300
 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile
 305 310 315 320
 Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335
 Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 340 345 350
 Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365
 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380
 Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400

Cys His

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1926 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: MURIDAE
 - (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 93..1289

(D) OTHER INFORMATION: /note= "mOP2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCAGGCACA GGTGCGCCGT CTGGTCCTCC CCGTCTGGCG TCAGCCGAGC	50
CCGACCAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT	104
Met Ala Met Arg	
1	
CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC	152
Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
5 10 15 20	
GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA	200
Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
25 30 35	
GCG CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG	248
Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly	
40 45 50	
CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG	296
Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln	
55 60 65	
CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC	344
Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr	
70 75 80	
GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC	392
Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp	
85 90 95 100	
CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC	440
Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly	
105 110 115	
TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC	488
Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile	
120 125 130	
CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA	536
Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu	
135 140 145	
CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA	584
Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu	
150 155 160	

GTG	GTC	CAA	GAG	CAC	TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	632
Val	Val	Gln	Glu	His	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
165					170					175					180	
CTT	CAG	ACG	CTC	CGA	TCT	GGG	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAC	ATC	680
Leu	Gln	Thr	Leu	Arg	Ser	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Ile	
				185					190						195	
ACA	GCA	GCC	AGT	GAC	CGA	TGG	CTG	CTG	AAC	CAT	CAC	AAG	GAC	CTG	GGA	728
Thr	Ala	Ala	Ser	Asp	Arg	Trp	Leu	Leu	Asn	His	His	Lys	Asp	Leu	Gly	
			200					205					210			
CTC	CGC	CTC	TAT	GTG	GAA	ACC	GCG	GAT	GGG	CAC	AGC	ATG	GAT	CCT	GGC	776
Leu	Arg	Leu	Tyr	Val	Glu	Thr	Ala	Asp	Gly	His	Ser	Met	Asp	Pro	Gly	
		215					220					225				
CTG	GCT	GGT	CTG	CTT	GGA	CGA	CAA	GCA	CCA	CGC	TCC	AGA	CAG	CCT	TTC	824
Leu	Ala	Gly	Leu	Leu	Gly	Arg	Gln	Ala	Pro	Arg	Ser	Arg	Gln	Pro	Phe	
	230					235					240					
ATG	GTA	ACC	TTC	TTC	AGG	GCC	AGC	CAG	AGT	CCT	GTG	CGG	GCC	CCT	CGG	872
Met	Val	Thr	Phe	Phe	Arg	Ala	Ser	Gln	Ser	Pro	Val	Arg	Ala	Pro	Arg	
245					250					255					260	
GCA	GCG	AGA	CCA	CTG	AAG	AGG	AGG	CAG	CCA	AAG	AAA	ACG	AAC	GAG	CTT	920
Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln	Pro	Lys	Lys	Thr	Asn	Glu	Leu	
				265					270					275		
CCG	CAC	CCC	AAC	AAA	CTC	CCA	GGG	ATC	TTT	GAT	GAT	GGC	CAC	GGT	TCC	968
Pro	His	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Gly	His	Gly	Ser	
			280					285					290			
CGC	GGC	AGA	GAG	GTT	TGC	CGC	AGG	CAT	GAG	CTC	TAC	GTC	AGC	TTC	CGT	1016
Arg	Gly	Arg	Glu	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	
		295					300					305				
GAC	CTT	GGC	TGG	CTG	GAC	TGG	GTC	ATC	GCC	CCC	CAG	GGC	TAC	TCT	GCC	1064
Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	
	310					315					320					
TAT	TAC	TGT	GAG	GGG	GAG	TGT	GCT	TTC	CCA	CTG	GAC	TCC	TGT	ATG	AAC	1112
Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	
325					330					335					340	
GCC	ACC	AAC	CAT	GCC	ATC	TTG	CAG	TCT	CTG	GTG	CAC	CTG	ATG	AAG	CCA	1160
Ala	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	
				345					350					355		
GAT	GTT	GTC	CCC	AAG	GCA	TGC	TGT	GCA	CCC	ACC	AAA	CTG	AGT	GCC	ACC	1208
Asp	Val	Val	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	
			360					365					370			

TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC	1256
Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His	
375 380 385	
CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCG CCCAGCATCC	1309
Arg Asn Met Val Val Lys Ala Cys Gly Cys His	
390 395	
TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT	1369
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCTGCTA	1429
AAATTCTGGT CTTTCCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC	1489
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA	1549
ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC	1609
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAATTC TAAACTAGAT	1669
GATCTGGGCT CTCTGCACCA TTCATTGTGG CAGTTGGGAC ATTTTtagGT ATAACAGACA	1729
CATACACTTA GATCAATGCA TCGCTGTACT CCTTGAAATC AGAGCTAGCT TGTTAGAAAA	1789
AGAATCAGAG CCAGGTATAG CCGTGCATGT CATTAAATCCC AGCGCTAAAG AGACAGAGAC	1849
AGGAGAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAA	1909
AAAAAAAAAC GGAATTC	1926

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "mOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Met	Arg	Pro	Gly	Pro	Leu	Trp	Leu	Leu	Gly	Leu	Ala	Leu	Cys	
1				5					10					15		
Ala	Leu	Gly	Gly	Gly	His	Gly	Pro	Arg	Pro	Pro	His	Thr	Cys	Pro	Gln	
		20						25					30			
Arg	Arg	Leu	Gly	Ala	Arg	Glu	Arg	Arg	Asp	Met	Gln	Arg	Glu	Ile	Leu	Ala
		35					40					45				

Val	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Gln	Pro	Ala	Ala	
50					55					60					65	
Ala	Arg	Gln	Pro	Ala	Ser	Ala	Pro	Leu	Phe	Met	Leu	Asp	Leu	Tyr	His	Ala
				70					75					80		
Met	Thr	Asp	Asp	Asp	Asp	Gly	Gly	Pro	Pro	Gln	Ala	His	Leu	Gly	Arg	
		85					90					95				
Ala	Asp	Leu	Val	Met	Ser	Phe	Val	Asn	Met	Val	Glu	Arg	Asp	Arg	Thr	
	100					105					110					
Leu	Gly	Tyr	Gln	Glu	Pro	His	Trp	Lys	Glu	Phe	His	Phe	Asp	Leu	Thr	
115					120					125					130	
Gln	Ile	Pro	Ala	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	
				135					140					145		
Lys	Glu	Pro	Ser	Thr	His	Pro	Leu	Asn	Thr	Thr	Leu	His	Ile	Ser	Met	
			150					155					160			
Phe	Glu	Val	Val	Gln	Glu	His	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	
		165					170					175				
Leu	Asp	Leu	Gln	Thr	Leu	Arg	Ser	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	
	180					185					190					
Asp	Ile	Thr	Ala	Ala	Ser	Asp	Arg	Trp	Leu	Leu	Asn	His	His	Lys	Asp	
195					200					205					210	
Leu	Gly	Leu	Arg	Leu	Tyr	Val	Glu	Thr	Ala	Asp	Gly	His	Ser	Met	Asp	
				215					220					225		
Pro	Gly	Leu	Ala	Gly	Leu	Leu	Gly	Arg	Gln	Ala	Pro	Arg	Ser	Arg	Gln	
			230					235						240		
Pro	Phe	Met	Val	Thr	Phe	Phe	Arg	Ala	Ser	Gln	Ser	Pro	Val	Arg	Ala	
		245					250					255				
Pro	Arg	Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln	Pro	Lys	Lys	Thr	Asn	
	260					265					270					
Glu	Leu	Pro	His	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Gly	His	
275					280					285					290	
Gly	Ser	Arg	Gly	Arg	Glu	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	
				295					300					305		
Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	
			310					315					320			

Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
325 330 335

Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
340 345 350

Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
355 360 365 370

Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
375 380 385

Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
390 395

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1368
- (D) OTHER INFORMATION: /STANDARD NAME="60A"

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: WHARTON, KRISTI A.; THOMSEN, GERALD H.; GELBERT, WILLIAM M.
- (B) TITLE: DROSOPHILA 60A GENE...
- (C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
- (D) VOLUME: 88
- (E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
- (F) PAGES: 9214-9218
- (G) DATE: OCT - 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG	TCG	GGA	CTG	CGA	AAC	ACC	TCG	GAG	GCC	GTT	GCA	GTG	CTC	GCC	TCC	48
Met	Ser	Gly	Leu	Arg	Asn	Thr	Ser	Glu	Ala	Val	Ala	Val	Leu	Ala	Ser	
1				5				10					15			

CTG	GGA	CTC	GGA	ATG	GTT	CTG	CTC	ATG	TTC	GTG	GCG	ACC	ACG	CCG	CCG	96
Leu	Gly	Leu	Gly	Met	Val	Leu	Leu	Met	Phe	Val	Ala	Thr	Thr	Pro	Pro	
			20					25					30			

GCC	GTT	GAG	GCC	ACC	CAG	TCG	GGG	ATT	TAC	ATA	GAC	AAC	GGC	AAG	GAC	144
Ala	Val	Glu	Ala	Thr	Gln	Ser	Gly	Ile	Tyr	Ile	Asp	Asn	Gly	Lys	Asp	
	35						40					45				
CAG	ACG	ATC	ATG	CAC	AGA	GTG	CTG	AGC	GAG	GAC	GAC	AAG	CTG	GAC	GTC	192
Gln	Thr	Ile	Met	His	Arg	Val	Leu	Ser	Glu	Asp	Asp	Lys	Leu	Asp	Val	
	50					55					60					
TCG	TAC	GAG	ATC	CTC	GAG	TTC	CTG	GGC	ATC	GCC	GAA	CGG	CCG	ACG	CAC	240
Ser	Tyr	Glu	Ile	Leu	Glu	Phe	Leu	Gly	Ile	Ala	Glu	Arg	Pro	Thr	His	
65					70					75					80	
CTG	AGC	AGC	CAC	CAG	TTG	TCG	CTG	AGG	AAG	TCG	GCT	CCC	AAG	TTC	CTG	288
Leu	Ser	Ser	His	Gln	Leu	Ser	Leu	Arg	Lys	Ser	Ala	Pro	Lys	Phe	Leu	
				85					90					95		
CTG	GAC	GTC	TAC	CAC	CGC	ATC	ACG	GCG	GAG	GAG	GGT	CTC	AGC	GAT	CAG	336
Leu	Asp	Val	Tyr	His	Arg	Ile	Thr	Ala	Glu	Glu	Gly	Leu	Ser	Asp	Gln	
		100						105					110			
GAT	GAG	GAC	GAC	GAC	TAC	GAA	CGC	GGC	CAT	CGG	TCC	AGG	AGG	AGC	GCC	384
Asp	Glu	Asp	Asp	Asp	Tyr	Glu	Arg	Gly	His	Arg	Ser	Arg	Arg	Ser	Ala	
		115					120					125				
GAC	CTC	GAG	GAG	GAT	GAG	GGC	GAG	CAG	CAG	AAG	AAC	TTC	ATC	ACC	GAC	432
Asp	Leu	Glu	Glu	Asp	Glu	Gly	Glu	Gln	Gln	Lys	Asn	Phe	Ile	Thr	Asp	
	130					135					140					
CTG	GAC	AAG	CGG	GCC	ATC	GAC	GAG	AGC	GAC	ATC	ATC	ATG	ACC	TTC	CTG	480
Leu	Asp	Lys	Arg	Ala	Ile	Asp	Glu	Ser	Asp	Ile	Ile	Met	Thr	Phe	Leu	
145					150					155					160	
AAC	AAG	CGC	CAC	CAC	AAT	GTG	GAC	GAA	CTG	CGT	CAC	GAG	CAC	GGC	CGT	528
Asn	Lys	Arg	His	His	Asn	Val	Asp	Glu	Leu	Arg	His	Glu	His	Gly	Arg	
				165					170					175		
CGC	CTG	TGG	TTC	GAC	GTC	TCC	AAC	GTG	CCC	AAC	GAC	AAC	TAC	CTG	GTG	576
Arg	Leu	Trp	Phe	Asp	Val	Ser	Asn	Val	Pro	Asn	Asp	Asn	Tyr	Leu	Val	
		180						185					190			
ATG	GCC	GAG	CTG	CGC	ATC	TAT	CAG	AAC	GCC	AAC	GAG	GGC	AAG	TGG	CTG	624
Met	Ala	Glu	Leu	Arg	Ile	Tyr	Gln	Asn	Ala	Asn	Glu	Gly	Lys	Trp	Leu	
	195						200					205				
ACC	GCC	AAC	AGG	GAG	TTC	ACC	ATC	ACG	GTA	TAC	GCC	ATT	GGC	ACC	GGC	672
Thr	Ala	Asn	Arg	Glu	Phe	Thr	Ile	Thr	Val	Tyr	Ala	Ile	Gly	Thr	Gly	
	210					215					220					
ACG	CTG	GGC	CAG	CAC	ACC	ATG	GAG	CCG	CTG	TCC	TCG	GTG	AAC	ACC	ACC	720
Thr	Leu	Gly	Gln	His	Thr	Met	Glu	Pro	Leu	Ser	Ser	Val	Asn	Thr	Thr	
225					230					235					240	

GGG Gly	GAC Asp	TAC Tyr	GTG Val	GGC Gly 245	TGG Trp	TTG Leu	GAG Glu	CTC Leu	AAC Asn 250	GTG Val	ACC Thr	GAG Glu	GGC Gly	CTG Leu 255	CAC His	768
GAG Glu	TGG Trp	CTG Leu	GTC Val 260	AAG Lys	TCG Ser	AAG Lys	GAC Asp	AAT Asn 265	CAT His	GGC Gly	ATC Ile	TAC Tyr	ATT Ile 270	GGA Gly	GCA Ala	816
CAC His	GCT Ala	GTC Val 275	AAC Asn	CGA Arg	CCC Pro	GAC Asp	CGC Arg 280	GAG Glu	GTG Val	AAG Lys	CTG Leu	GAC Asp 285	GAC Asp	ATT Ile	GGA Gly	864
CTG Leu	ATC Ile 290	CAC His	CGC Arg	AAG Lys	GTG Val	GAC Asp 295	GAC Asp	GAG Glu	TTC Phe	CAG Gln	CCC Pro 300	TTC Phe	ATG Met	ATC Ile	GGC Gly	912
TTC Phe 305	TTC Phe	CGC Arg	GGA Gly	CCG Pro	GAG Glu 310	CTG Leu	ATC Ile	AAG Lys	GCG Ala	ACG Thr 315	GCC Ala	CAC His	AGC Ser	AGC Ser	CAC His 320	960
CAC His	AGG Arg	AGC Ser	AAG Lys	CGA Arg 325	AGC Ser	GCC Ala	AGC Ser	CAT His	CCA Pro 330	CGC Arg	AAG Lys	CGC Arg	AAG Lys	AAG Lys 335	TCG Ser	1008
GTG Val	TCG Ser	CCC Pro	AAC Asn 340	AAC Asn	GTG Val	CCG Pro	CTG Leu	CTG Leu 345	GAA Glu	CCG Pro	ATG Met	GAG Glu	AGC Ser 350	ACG Thr	CGC Arg	1056
AGC Ser	TGC Cys	CAG Gln 355	ATG Met	CAG Gln	ACC Thr	CTG Leu	TAC Tyr 360	ATA Ile	GAC Asp	TTC Phe	AAG Lys	GAT Asp 365	CTG Leu	GGC Gly	TGG Trp	1104
CAT His	GAC Asp 370	TGG Trp	ATC Ile	ATC Ile	GCA Ala	CCA Pro 375	GAG Glu	GGC Gly	TAT Tyr	GGC Gly	GCC Ala 380	TTC Phe	TAC Tyr	TGC Cys	AGC Ser	1152
GGC Gly 385	GAG Glu	TGC Cys	AAT Asn	TTC Phe	CCG Pro 390	CTC Leu	AAT Asn	GCG Ala	CAC His	ATG Met 395	AAC Asn	GCC Ala	ACG Thr	AAC Asn 400	CAT His	1200
GCG Ala	ATC Ile	GTC Val	CAG Gln	ACC Thr 405	CTG Leu	GTC Val	CAC His	CTG Leu 410	CTG Leu	GAG Glu	CCC Pro	AAG Lys	AAG Lys	GTG Val 415	CCC Pro	1248
AAG Lys	CCC Pro	TGC Cys	TGC Cys 420	GCT Ala	CCG Pro	ACC Thr	AGG Arg	CTG Leu 425	GGA Gly	GCA Ala	CTA Leu	CCC Pro	GTT Val 430	CTG Leu	TAC Tyr	1296
CAC His	CTG Leu	AAC Asn 435	GAC Asp	GAG Glu	AAT Asn	GTG Val	AAC Asn 440	CTG Leu	AAA Lys	AAG Lys	TAT Tyr	AGA Arg 445	AAC Asn	ATG Met	ATT Ile	1344

GTG AAA TCC TGC GGG TGC CAT TGA
Val Lys Ser Cys Gly Cys His
450 455

1368

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
1 5 10 15
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro
20 25 30
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp
35 40 45
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val
50 55 60
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His
65 70 75 80
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu
85 90 95
Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln
100 105 110
Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala
115 120 125
Asp Leu Glu Glu Asp Glu Gly Gly Gln Gln Lys Asn Phe Ile Thr Asp
130 135 140
Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu
145 150 155 160
Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg
165 170 175
Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val
180 185 190

Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu
195 200 205

Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly
210 215 220

Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr
225 230 235 240

Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His
245 250 255

Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala
260 265 270

His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly
275 280 285

Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly
290 295 300

Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His
305 310 315 320

His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser
325 330 335

Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg
340 345 350

Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
355 360 365

His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
370 375 380

Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
385 390 395 400

Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
405 410 415

Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
420 425 430

His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
435 440 445

Val Lys Ser Cys Gly Cys His
450 455

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: /note="BMP3"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys	Ala	Arg	Arg	Tyr	Leu	Lys	Val	Asp	Phe	Ala	Asp	Ile	Gly	Trp	Ser
1				5					10					15	
Glu	Trp	Ile	Ile	Ser	Pro	Lys	Ser	Phe	Asp	Ala	Tyr	Try	Cys	Ser	Gly
			20					25					30		
Ala	Cys	Gln	Phe	Pro	Met	Pro	Lys	Ser	Leu	Lys	Pro	Ser	Asn	His	Ala
		35					40					45			
Thr	Ile	Gln	Ser	Ile	Val	Ala	Arg	Ala	Val	Gly	Val	Val	Pro	Gly	Ile
		50				55				60					

Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
65 70 75 80
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
85 90 95
Thr Val Glu Ser Cys Ala Cys Arg
100

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1 5 10 15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20 25 30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
50 55 60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80
Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85 90 95
Arg Ser Cys Gly Cys His
100

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys	Arg	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Gln	1	5	10	15
Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp	Gly	20	25	30	
Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala	35	40	45	
Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	Pro	Glu	Tyr	Val	Pro	Lys	50	55	60	
Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	65	70	75	80
Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Trp	Met	Val	Val	85	90	95	
Arg	Ala	Cys	Gly	Cys	His	100													

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..102

(D) OTHER INFORMATION: /label= OPX

/note= "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY
SELECTED FROM THE RESIDUES OCCURRING AT THE
CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE
OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or
16,18,20 and 22.)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1          5          10          15
Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20          25          30
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35          40          45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
50          55          60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65          70          75          80
Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85          90          95
Xaa Ala Cys Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:30:

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

(A) NAME: Generic Sequence 5

(D) OTHER INFORMATION: wherein each Xaa is independently
selected from a group of one or more specified amino acids as
defined in the specification.

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Leu Xaa Xaa Xaa Phe
1          5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
10

```

```

Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 15                20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 25                30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
                35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
 40                45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                50
Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55                60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 65
Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70                75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
                80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 85                90
Xaa Cys Xaa Cys Xaa
 95

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: Generic Sequence 6
- (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
 1                5                10
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
                15
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 20                25
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 30                35
Xaa Pro Xaa Xaa Xaa Xaa Xaa
                40
Xaa Xaa Xaa Asn His Ala Xaa Xaa
 45                50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                55

```

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
	60					65	
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa
			70				
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	
	75				80		
Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa
			85				
Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa
	90				95		
Xaa	Cys	Xaa	Cys	Xaa			
		100					

(2) INFORMATION FOR SEQ ID NO:32:

- ```

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1238 base pairs, 372 amino acids
(B) TYPE: nucleic acid, amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) ORIGINAL SOURCE:
(A) ORGANISM: human
(F) TISSUE TYPE: BRAIN

(iv) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:
(D) OTHER INFORMATION:
 /product= "GDF-1"
 /note= "GDF-1 CDNA"

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Lee, Se-Jin
(B) TITLE: Expression of Growth/Differentiation Factor 1
(C) JOURNAL: Proc. Nat'l Acad. Sci.
(D) VOLUME: 88
(E) RELEVANT RESIDUES: 1-1238
(F) PAGES: 4250-4254
(G) DATE: May-1991
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

GGGGACACCG GCCCGCCCT CAGCCCACTG GTCCCGGGCC GCCCGGACC CTGCGCACTC 60

TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC 113

Met Pro Pro Pro Gln Gln Gly Pro Cys Gly

1 5 10



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAC | CAC | CTC | CTC | CTC | CTC | CTG | GCC | CTG | CTG | CTG | CCC | TCG | CTG | CCC | 158 |
| His | His | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Leu | Leu | Pro | Ser | Leu | Pro |     |
|     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |
| CTG | ACC | CGC | GCC | CCC | GTG | CCC | CCA | GGC | CCA | GCC | GCC | GCC | CTG | CTC | 203 |
| Leu | Thr | Arg | Ala | Pro | Val | Pro | Pro | Gly | Pro | Ala | Ala | Ala | Leu | Leu |     |
|     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |
| CAG | GCT | CTA | GGA | CTG | CGC | GAT | GAG | CCC | CAG | GGT | GCC | CCC | AGG | CTC | 248 |
| Gln | Ala | Leu | Gly | Leu | Arg | Asp | Glu | Pro | Gln | Gly | Ala | Pro | Arg | Leu |     |
|     |     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |
| CGG | CCG | GTT | CCC | CCG | GTC | ATG | TGG | CGC | CTG | TTT | CGA | CGC | CGG | GAC | 293 |
| Arg | Pro | Val | Pro | Pro | Val | Met | Trp | Arg | Leu | Phe | Arg | Arg | Arg | Asp |     |
|     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |
| CCC | CAG | GAG | ACC | AGG | TCT | GGC | TCG | CGG | CGG | ACG | TCC | CCA | GGG | GTC | 338 |
| Pro | Gln | Glu | Thr | Arg | Ser | Gly | Ser | Arg | Arg | Thr | Ser | Pro | Gly | Val |     |
|     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |
| ACC | CTG | CAA | CCG | TGC | CAC | GTG | GAG | GAG | CTG | GGG | GTC | GCC | GGA | AAC | 383 |
| Thr | Leu | Gln | Pro | Cyc | His | Val | Glu | Glu | Leu | Gly | Val | Ala | Gly | Asn |     |
|     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |
| ATC | GTG | CGC | CAC | ATC | CCG | GAC | CGC | GGT | GCG | CCC | ACC | CGG | GCC | TCG | 428 |
| Ile | Val | Arg | His | Ile | Pro | Asp | Arg | Gly | Ala | Pro | Thr | Arg | Ala | Ser |     |
|     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |
| GAG | CCT | GTC | TCG | GCC | GCG | GGG | CAT | TGC | CCT | GAG | TGG | ACA | GTC | GTC | 473 |
| Glu | Pro | Val | Ser | Ala | Ala | Gly | His | Cys | Pro | Glu | Trp | Thr | Val | Val |     |
|     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |
| TTC | GAC | CTG | TCG | GCT | GTG | GAA | CCC | GCT | GAG | CGC | CCG | AGC | CGG | GCC | 518 |
| Phe | Asp | Leu | Ser | Ala | Val | Glu | Pro | Ala | Glu | Arg | Pro | Ser | Arg | Ala |     |
|     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |
| CGC | CTG | GAG | CTG | CGT | TTC | GCG | GCG | GCG | GCG | GCG | GCA | GCC | CCG | GAG | 563 |
| Arg | Leu | Glu | Leu | Arg | Phe | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Pro | Glu |     |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| GGC | GGC | TGG | GAG | CTG | AGC | GTG | GCG | CAA | GCG | GGC | CAG | GGC | GCG | GGC | 608 |
| Gly | Gly | Trp | Glu | Leu | Ser | Val | Ala | Gln | Ala | Gly | Gln | Gly | Ala | Gly |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| GCG | GAC | CCC | GGG | CCG | GTG | CTG | CTC | CGC | CAG | TTG | GTG | CCC | GCC | CTG | 653 |
| Ala | Asp | Pro | Gly | Pro | Val | Leu | Leu | Arg | Gln | Leu | Val | Pro | Ala | Leu |     |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| GGG | CCG | CCA | GTG | CGC | GCG | GAG | CTG | CTG | GGC | GCC | GCT | TGG | GCT | CGC | 698 |
| Gly | Pro | Pro | Val | Arg | Ala | Glu | Leu | Leu | Gly | Ala | Ala | Trp | Ala | Arg |     |
|     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |

[illegible]

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human  
(F) TISSUE TYPE: BRAIN

(ix) **FEATURE:**

- (A) NAME/KEY: CDS  
(B) LOCATION:  
(D) OTHER INFORMATION: /function=  
/product= "GDF-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Val | Ser | Ala | Ala | Gly | His | Cys | Pro | Glu | Trp | Thr | Val | Val | 120 | 125 | 130 |
| Phe | Asp | Leu | Ser | Ala | Val | Glu | Pro | Ala | Glu | Arg | Pro | Ser | Arg | Ala | 135 | 140 | 145 |
| Arg | Leu | Glu | Leu | Arg | Phe | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Pro | Glu | 150 | 155 | 160 |
| Gly | Gly | Trp | Glu | Leu | Ser | Val | Ala | Gln | Ala | Gly | Gln | Gly | Ala | Gly | 165 | 170 | 175 |
| Ala | Asp | Pro | Gly | Pro | Val | Leu | Leu | Arg | Gln | Leu | Val | Pro | Ala | Leu | 180 | 185 | 190 |
| Gly | Pro | Pro | Val | Arg | Ala | Glu | Leu | Leu | Gly | Ala | Ala | Trp | Ala | Arg | 195 | 200 | 205 |
| Asn | Ala | Ser | Trp | Pro | Arg | Ser | Leu | Arg | Leu | Ala | Leu | Ala | Leu | Arg | 210 | 215 | 220 |
| Pro | Arg | Ala | Pro | Ala | Ala | Cys | Ala | Arg | Leu | Ala | Glu | Ala | Ser | Leu | 225 | 230 | 235 |
| Leu | Leu | Val | Thr | Leu | Asp | Pro | Arg | Leu | Cys | His | Pro | Leu | Ala | Arg | 240 | 245 | 250 |
| Pro | Arg | Arg | Asp | Ala | Glu | Pro | Val | Leu | Gly | Gly | Gly | Pro | Gly | Gly | 255 | 260 | 265 |
| Ala | Cys | Arg | Ala | Arg | Arg | Leu | Tyr | Val | Ser | Phe | Arg | Glu | Val | Gly | 270 | 275 | 280 |
| Trp | His | Arg | Trp | Val | Ile | Arg | Pro | Arg | Gly | Phe | Leu | Ala | Asn | Tyr | 285 | 290 | 295 |
| Cys | Gln | Gly | Gln | Cys | Ala | Leu | Pro | Val | Ala | Leu | Ser | Gly | Ser | Gly | 300 | 305 | 310 |
| Gly | Pro | Pro | Ala | Leu | Asn | His | Ala | Val | Leu | Arg | Ala | Leu | Met | His | 315 | 320 | 325 |
| Ala | Ala | Ala | Pro | Gly | Ala | Ala | Asp | Leu | Pro | Cys | Cys | Val | Pro | Ala | 330 | 335 | 340 |
| Arg | Leu | Ser | Pro | Ile | Ser | Val | Leu | Phe | Phe | Asp | Asn | Ser | Asp | Asn | 345 | 350 | 355 |
| Val | Val | Leu | Arg | Gln | Tyr | Glu | Asp | Met | Val | Val | Asp | Glu | Cys | Gly | 360 | 365 | 370 |
| Cys | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     | 372 |     |     |